

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/965,313

DATE: 10/18/2001
TIME: 16:18:36

Input Set : A:\Sequencing Listing as filed.txt
Output Set: N:\CRF3\10182001\I965313.raw

ENTERED

f 2

4 <110> APPLICANT: Hodge, Martin R.
6 <120> TITLE OF INVENTION: Novel IL-9/IL-2 Receptor-Like Molecules
7 and Uses Thereof
9 <130> FILE REFERENCE: 5800-17A
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/965,313
C--> 11 <141> CURRENT FILING DATE: 2001-09-26
11 <150> PRIOR APPLICATION NUMBER: US 09/313,913
12 <151> PRIOR FILING DATE: 1999-05-18
14 <160> NUMBER OF SEQ ID NOS: 8
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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19 <211> LENGTH: 2343
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (349)...(1962)
27 <400> SEQUENCE: 1
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29 cgcctgtac cttcccttgcgt ctctcttcc tctgtctgtc gctctgtggg acacccgtcct 120
30 ggaggcccaag ctggccgtca tcagagtgac aggtcttatg acagccgtat tggtgactcg 180
31 ggctgggtgt ggattctcac cccaggcctc tgccctgttt ctcagacccat catctgtcac 240
32 ccccacgctg aaccaggctg ccaccccccag aagcccatca gactgcccccc agcacacgg 300
33 atggatttct gagaagaagaag ccgaaacacaaggccctgg gagtcagc atg ccg cgt 357
34 Met Pro Arg
35 1
37 ggc tgg gcc ccc ctg ctc ctg ctg ctc cag gga ggc tgg ggc 405
38 Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly Gly Trp Gly
39 5 10 15
41 tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag acg gtc atc tgc 453
42 Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr Val Ile Cys
43 20 25 30 35
45 atc ctg gaa atg tgg aac ctc cac ccc acg ctc acc ctt acc tgg 501
46 Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp
47 40 45 50
49 caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc tgc agc ctc 549
50 Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu
51 55 60 65
53 cac agg tcg gcc cac aat gcc acg cat gcc acc tac acc tgc cac atg 597
54 His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met
55 70 75 80
57 gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc aac atc aca 645
58 Asp Val Phe His Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr
59 85 90 95
61 gac cag tct ggc aac tac tcc cag gag tgg ggc agc ttt ctc ctg gct 693
62 Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala
63 100 105 110 115

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65	gag	agc	atc	aag	ccg	gct	ccc	cct	ttc	aac	gtg	act	gtg	acc	ttc	tca	741		
66	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Phe	Asn	Val	Thr	Val	Thr	Phe	Ser			
67																120	125	130	
69	gga	cag	tat	aat	atc	tcc	tgg	cgc	tca	gat	tac	gaa	gac	cct	gcc	ttc	789		
70	Gly	Gln	Tyr	Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp	Pro	Ala	Phe			
71																135	140	145	
73	tac	atg	ctg	aag	ggc	aag	ctt	cag	tat	gag	ctg	cag	tg	agg	aac	cg	837		
74	Tyr	Met	Leu	Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr	Arg	Asn	Arg			
75																150	155	160	
77	gga	gac	ccc	tgg	gct	gtg	agt	ccg	agg	aga	aag	ctg	atc	tca	gtg	gac	885		
78	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	Ile	Ser	Val	Asp			
79																165	170	175	
81	tca	aga	agt	gtc	tcc	ctc	ccc	ctg	gag	ttc	ccg	aaa	gac	tcg	agc	933			
82	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	Leu	Glu	Phe	Arg	Lys	Asp	Ser	Ser			
83																180	185	190	195
85	tat	gag	ctg	cag	gtg	ccg	gca	ggg	ccc	atg	cct	ggc	tcc	tcc	tac	cag	981		
86	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	Pro	Met	Pro	Gly	Ser	Ser	Tyr	Gln			
87																200	205	210	
89	ggg	acc	tgg	agt	gaa	tgg	agt	gac	ccg	gtc	atc	ttt	cag	acc	cag	tca	1029		
90	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	Gln	Thr	Gln	Ser			
91																215	220	225	
93	gag	gag	tta	aag	gaa	ggc	tgg	aac	cct	cac	ctg	ctg	ctt	ctc	ctc	ctg	1077		
94	Glu	Glu	Leu	Lys	Glu	Gly	Trp	Asn	Pro	His	Leu	Leu	Leu	Leu	Leu	Leu			
95																230	235	240	
97	ctt	gtc	ata	gtc	tcc	att	cct	gcc	tcc	ttc	tgg	agc	ctg	aag	acc	cat	1125		
98	Leu	Val	Ile	Val	Phe	Ile	Pro	Ala	Phe	Trp	Ser	Leu	Lys	Thr	His	Pro			
99																245	250	255	
101	ttg	tgg	agg	cta	tgg	aag	aag	ata	tgg	gcc	gtc	ccc	agc	cct	gag	cg	1173		
102	Leu	Trp	Arg	Leu	Trp	Lys	Lys	Ile	Trp	Ala	Val	Pro	Ser	Pro	Glu	Arg			
103																260	265	270	275
105	ttc	tcc	atg	ccc	ctg	tac	aag	ggc	tgc	agc	gga	gac	tcc	aag	aaa	tgg	1221		
106	Phe	Phe	Met	Pro	Leu	Tyr	Lys	Gly	Cys	Ser	Gly	Asp	Phe	Lys	Lys	Trp			
107																280	285	290	
109	gtg	gg	gca	ccc	tcc	act	ggc	tcc	agc	ctg	gag	ctg	gga	ccc	tgg	agc	1269		
110	Val	Gly	Ala	Pro	Phe	Thr	Gly	Ser	Ser	Leu	Glu	Leu	Gly	Pro	Trp	Ser			
111																295	300	305	
113	cca	gag	gt	ccc	tcc	acc	ctg	gag	gt	tac	agc	tgc	cac	cca	ccg	1317			
114	Pro	Glu	Val	Pro	Ser	Thr	Leu	Glu	Val	Tyr	Ser	Cys	His	Pro	Pro	Arg			
115																310	315	320	
117	agc	ccg	gcc	aag	agg	ctg	cag	ctc	acg	gag	cta	caa	gaa	cca	gca	gag	1365		
118	Ser	Pro	Ala	Lys	Arg	Leu	Gln	Leu	Thr	Glu	Leu	Gln	Glu	Pro	Ala	Glu			
119																325	330	335	
121	ctg	gt	gag	tct	gac	gg	gt	ccc	aag	ccc	agc	tcc	tgg	ccg	aca	gc	1413		
122	Leu	Val	Glu	Ser	Asp	Gly	Val	Pro	Lys	Pro	Ser	Phe	Trp	Pro	Thr	Ala			
123																340	345	350	355
125	cag	aac	tcg	ggg	ggc	tca	gct	tac	agt	gag	tg	gag	agg	gat	cg	cc	1461		
126	Gln	Asn	Ser	Gly	Gly	Ser	Ala	Tyr	Ser	Glu	Glu	Arg	Asp	Arg	Pro	Tyr			
127																360	365	370	
129	ggc	ctg	gt	tcc	att	gac	aca	gt	act	gt	ct	gat	gca	gag	gg	cc	1509		

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130	Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala Glu Gly Pro			
131	375	380	385	
133	tgc acc tgg ccc tgc agc tgt gag gat gac ggc tac cca gcc ctg gac			1557
134	Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Leu Asp			
135	390	395	400	
137	ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac cca ctc ttg			1605
138	Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp Pro Leu Leu			
139	405	410	415	
141	gat gca ggg acc aca gtc ctg tcc tgt ggc tgc tca gct ggc agc			1653
142	Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser Ala Gly Ser			
143	420	425	430	435
145	cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga cta aag cca			1701
146	Pro Gly Leu Gly Pro Leu Gly Ser Leu Leu Asp Arg Leu Lys Pro			
147	440	445	450	
149	ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc tgg ggt ggc			1749
150	Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro Trp Gly Gly			
151	455	460	465	
153	cgg tca cct gga ggg gtc tca gag agt gag gcg ggc tca ccc ctg gcc			1797
154	Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser Pro Leu Ala			
155	470	475	480	
157	ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc tct gac tgc			1845
158	Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly Ser Asp Cys			
159	485	490	495	
161	agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac gaa gga ccc			1893
162	Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu Gly Pro			
163	500	505	510	515
165	ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg cca ctt tcg			1941
166	Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro Leu Ser			
167	520	525	530	
169	agc cct gga ccc cag gcc agc taatgaggct gactggatgt ccagagctgg			1992
170	Ser Pro Gly Pro Gln Ala Ser			
171	535			
173	ccagggccact gggccctgag ccagagacaa ggtcacctgg gctgtatgt gaagacacct			2052
174	gcagcccttg gtcctctgga tggccctttg agcctgtatgt ttacagtgtc tgggtgtgt			2112
175	tgtgcatacg tggatgtgtg catatgcatacg tggatgtgtg tggatgtgtt agtgcgcag			2172
176	tggatgtcc acgtgtgtgt gtgattgcac gtgcctgtgg gcctggata atccccatgg			2232
177	tactccatgc attcacctgc cctgtgcatacg tctggactca cggagctcac ccatgtgcac			2292
178	aagtgtgcac agtaaacgtg tttgtgtca aaaaaaaaaa aaaaaaaaaa a			2343
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181	<211> LENGTH: 538			
182	<212> TYPE: PRT			
183	<213> ORGANISM: Homo sapiens IL-2/IL-9 Receptor Like			
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187	1	5	10	15
188	Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr			
189	20	25	30	
190	Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr			
191	35	40	45	

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192 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
193 50 55 60
194 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
195 65 70 75 80
196 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
197 85 90 95
198 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
199 100 105 110
200 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
201 115 120 125
202 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
203 130 135 140
204 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
205 145 150 155 160
206 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
207 165 170 175
208 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
209 180 185 190
210 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
211 195 200 205
212 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
213 210 215 220
214 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu
215 225 230 235 240
216 Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys
217 245 250 255
218 Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser
219 260 265 270
220 Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe
221 275 280 285
222 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly
223 290 295 300
224 Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
225 305 310 315 320
226 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu
227 325 330 335
228 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp
229 340 345 350
230 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp
231 355 360 365
232 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
233 370 375 380
234 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
235 385 390 395 400
236 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
237 405 410 415
238 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
239 420 425 430
240 Ala Gly Ser Pro Gly Leu Gly Pro Leu Gly Ser Leu Leu Asp Arg

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241      435          440          445
242  Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
243      450          455          460
244  Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser
245      465          470          475          480
246  Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly
247      485          490          495
248  Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp
249      500          505          510
250  Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro
251      515          520          525
252  Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
253      530          535
255 <210> SEQ ID NO: 3
256 <211> LENGTH: 2456
257 <212> TYPE: DNA
258 <213> ORGANISM: Mus musculus
260 <220> FEATURE:
261 <221> NAME/KEY: CDS
262 <222> LOCATION: (391)...(1977)
264 <400> SEQUENCE: 3
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266 gtctgccat ccctggggca gccaactggc ctcagcccg tgcctgtct      120
267 ctgtctggct gccccagccc tactgtctc ctctgtgttag gctctgccc gatgcccggc      180
268 tggtcctcag cctcaggact atctcagcag tgactccct gattctggac ttgcacctga      240
269 ctgaacctct gcccacctca aaccttcaacc tcccaccacc accactccga gtcccgctgt      300
270 gactcccacg cccaggagac cacccaaatg ccccagccata aagaatggct ttctgaggaa      360
271 gatcctgaag gagtaggtct gggacacagc atg ccc cgg ggc cca gtg gct gcc      414
272                               Met Pro Arg Gly Pro Val Ala Ala
273                               1           5
275 tta ctc ctg ctg att ctc cat gga gct tgg agc tgc ctg gac ctc act      462
276 Leu Leu Leu Ile Leu His Gly Ala Trp Ser Cys Leu Asp Leu Thr
277      10          15          20
279 tgc tac act gac tac ctc tgg acc atc acc tgt gtc ctg gag aca cgg      510
280 Cys Tyr Thr Asp Tyr Leu Trp Thr Ile Thr Cys Val Leu Glu Thr Arg
281      25          30          35          40
283 agc ccc aac ccc agc ata ctc agt ctc acc tgg caa gat gaa tat gag      558
284 Ser Pro Asn Pro Ser Ile Leu Ser Leu Thr Trp Gln Asp Glu Tyr Glu
285      45          50          55
287 gaa ctt cag gac caa gag acc ttc tgc agc cta cac aag tct ggc cac      606
288 Glu Leu Gln Asp Gln Glu Thr Phe Cys Ser Leu His Lys Ser Gly His
289      60          65          70
291 aac acc aca cat ata tgg tac acg tgc cat atg cgc ttg tct caa ttc      654
292 Asn Thr Thr His Ile Trp Tyr Thr Cys His Met Arg Leu Ser Gln Phe
293      75          80          85
295 ctg tcc gat gaa gtt ttc att gtc aac gtg acg gac cag tct ggc aac      702
296 Leu Ser Asp Glu Val Phe Ile Val Asn Val Thr Asp Gln Ser Gly Asn
297      90          95          100
299 aac tcc caa gag tgc gtc gct gac atc aag cca      750

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date